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## SEQUENCE LISTING

<110> PLOWMAN, GREGORY D.  
WHYTE, DAVID  
MARTINEZ, RICARDO  
HILL, RONALD  
FLANAGAN, PETER  
LIOUBIN, MARIO

<120> NOVEL PROTEIN PHOSPHATASES AND DIAGNOSIS AND TREATMENT  
OF PHOSPHATASE-RELATED DISORDERS

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<140> 10/049,515  
<141> 2002-06-14

<150> PCT/US00/22158  
<151> 2000-08-11

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<170> PatentIn Ver. 3.2

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Asp Gln Gly Val Arg His Leu Val Ser Leu Thr Glu Arg Gly Pro Pro  
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 35 40 45

Gly Pro Arg Ala Pro Gly Val Ala Glu Leu Arg Val Pro Val Phe Asp  
 50 55 60

Asp Pro Ala Glu Asp Leu Leu Thr His Leu Glu Pro Thr Cys Ala Ala  
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Met Glu Ala Ala Val Arg Asp Gly Gly Ser Cys Leu Val Tyr Cys Lys  
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Asn Gly Arg Ser Arg Ser Ala Ala Val Cys Thr Ala Tyr Leu Met Arg  
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His Arg Gly His Ser Leu Asp Arg Ala Phe Gln Met Val Lys Ser Ala  
 115 120 125

Arg Pro Val Ala Glu Pro Asn Leu Gly Phe Trp Ala Gln Leu Gln Lys  
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Lys Tyr Leu Cys Ile Pro Ala Ala Asp Thr Pro Ser Gln Asn Leu Thr  
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Arg His Phe Lys Glu Ser Ile Lys Phe Ile His Glu Cys Arg Leu Gln  
65 70 75 80  
Gly Glu Ser Cys Leu Val His Cys Leu Ala Gly Val Ser Arg Ser Val  
85 90 95  
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100 105 110  
Asp Ala Leu His Thr Val Arg Ala Gly Arg Ser Cys Ala Asn Pro Asn  
115 120 125  
Leu Gly Phe Gln Arg Gln Leu Gln Glu Phe Glu Lys His Glu Val His  
130 135 140  
Gln Tyr Arg Gln Trp Leu Arg Glu Glu Tyr Gly Glu Asn Pro Leu Arg  
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Arg Leu Leu Trp Val Arg Arg Thr Ala Thr Leu Thr His Ile Asn Glu  
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Val Trp Pro Asn Leu Phe Leu Gly Asp Ala Tyr Ala Ala Arg Asp Lys  
50 55 60  
Gly Arg Leu Ile Gln Leu Gly Ile Thr His Val Val Asn Val Ala Ala  
65 70 75 80  
Gly Lys Phe Gln Val Asp Thr Gly Ala Lys Phe Tyr Arg Gly Thr Pro  
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Leu Glu Tyr Tyr Gly Ile Glu Ala Asp Asp Asn Pro Phe Phe Asp Leu  
100 105 110  
Ser Val His Phe Leu Pro Val Ala Arg Tyr Ile Arg Asp Ala Leu Asn  
115 120 125  
Ile Pro Arg Ser Arg Val Leu Val His Cys Ala Met Gly Val Ser Arg  
130 135 140  
Ser Ala Thr Ile Val Leu Ala Phe Leu Met Ile Phe Glu Asn Met Thr  
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 35 40 45  
 Gly Gly Gly Cys Gly Tyr Val Gln Asp Leu Thr Leu Asp Leu Gln  
 50 55 60  
 Val Gly Val Ile Lys Pro Trp Leu Leu Leu Gly Ser Gln Asp Ala Ala  
 65 70 75 80  
 His Asp Leu Glu Leu Leu Arg Lys His Lys Val Thr His Ile Leu Asn  
 85 90 95  
 Val Ala Tyr Gly Val Glu Asn Ala Phe Leu Ser Glu Phe Thr Tyr Lys  
 100 105 110  
 Thr Ile Ser Ile Leu Asp Val Pro Glu Thr Asn Ile Leu Ser Tyr Phe  
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 Pro Glu Cys Phe Glu Phe Ile Glu Gln Ala Lys Leu Lys Asp Gly Val  
 130 135 140  
 Val Leu Val His Cys Asn Ala Gly Val Ser Arg Ala Ala Ala Ile Val  
 145 150 155 160  
 Ile Gly Phe Leu Met Ser Ser Glu Glu Ala Thr Phe Thr Thr Ala Leu  
 165 170 175  
 Ser Leu Val Lys Glu Ala Arg Pro Ser Ile Cys Pro Asn Pro Gly Phe  
 180 185 190  
 Met Glu Gln Leu Arg Thr Tyr Gln Val Gly Lys Glu Ser Asn Gly Gly  
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His Ile Leu Ser Val His Asp Ser Ala Arg Pro Met Leu Glu Gly Val  
35 40 45

Lys Tyr Leu Cys Ile Pro Ala Ala Asp Ser Pro Ser Gln Asn Leu Thr  
50 55 60

Arg His Phe Lys Glu Ser Ile Lys Phe Ile His Glu Cys Arg Leu Arg  
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 Gly Glu Ser Cys Leu Val His Cys Leu Ala Gly Val Ser Arg Ser Val  
 85 90 95  
 Thr Leu Val Ile Ala Tyr Ile Met Thr Val Thr Asp Phe Gly Trp Glu  
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 Asp Ala Leu His Thr Val Arg Ala Gly Arg Ser Cys Ala Asn Pro Asn  
 115 120 125  
 Val Gly Phe Gln Arg Gln Leu Gln Glu Phe Glu Lys His Glu Val His  
 130 135 140  
 Gln Tyr Arg Gln Trp Leu Lys Glu Glu Tyr Gly Glu Ser Pro Leu Gln  
 145 150 155 160  
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Gly Gly Gly Ala Ser Ala Ala Ser Ser Met Leu Pro Gln Ser Val Pro  
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 50 55 60

Leu Phe Leu Gly Asn Glu Gln Asp Ala Gln Asp Leu Asp Thr Met Gln  
 65 70 75 80

Arg Leu Asn Ile Gly Tyr Val Ile Asn Val Thr Thr His Leu Pro Leu  
 85 90 95

Tyr His Tyr Glu Lys Gly Leu Phe Asn Tyr Lys Arg Leu Pro Ala Thr  
 100 105 110

Asp Ser Asn Lys Gln Asn Leu Arg Gln Tyr Phe Glu Glu Ala Phe Glu  
 115 120 125

Phe Ile Glu Glu Ala His Gln Cys Gly Lys Gly Leu Leu Ile His Cys  
 130 135 140

Gln Ala Gly Val Ser Arg Ser Ala Thr Ile Val Ile Ala Tyr Leu Met  
 145 150 155 160

Lys His Thr Arg Met Thr Met Thr Asp Ala Tyr Lys Phe Val Lys Gly  
 165 170 175

Lys Arg Pro Ile Ile Ser Pro Asn Leu Asn Phe Met Gly Gln Leu Leu  
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 20 25 30  
 Gly Leu Tyr Leu Gly Gly Ala Ala Ala Val Ala Glu Pro Gly His Leu  
 35 40 45  
 Arg Glu Ala Gly Ile Thr Ala Val Leu Thr Val Asp Ser Glu Pro Ala  
 50 55 60  
 Phe Pro Ala Gly Ala Gly Phe Glu Gly Leu Arg Ser Leu Phe Val Pro  
 65 70 75 80  
 Ala Leu Asp Lys Pro Glu Thr Asp Leu Leu Ser His Leu Asp Arg Cys  
 85 90 95  
 Val Ala Phe Ile Gly Gln Ala Arg Ser Glu Gly Arg Ala Val Leu Val  
 100 105 110  
 His Cys His Ala Gly Val Ser Arg Ser Val Ala Val Val Met Ala Phe  
 115 120 125  
 Ile Met Lys Thr Asp Gln Leu Thr Phe Glu Lys Ala Tyr Asp Ile Leu  
 130 135 140  
 Arg Thr Val Lys Pro Glu Ala Lys Val Asn Glu Gly Phe Glu Trp Gln  
 145 150 155 160  
 Leu Lys Leu Tyr Glu Ala Met Gly Tyr Glu Val Asp Thr Ser Ser Ala  
 165 170 175  
 Phe Tyr Lys Gln Tyr Arg Leu Gln Lys Val Thr Glu Lys Tyr Pro Glu  
 180 185 190  
 Leu Trp Asn Leu Pro Gln Glu Leu Phe Ala Val Asp Pro Thr Thr Ile  
 195 200 205

Ser Gln Gly Leu Lys Asp Asp Ile Leu Tyr Lys Cys Arg Lys Cys Arg  
 210 215 220  
 Arg Ser Leu Phe Arg His Ser Ser Ile Leu Gly His Ser Glu Gly Ser  
 225 230 235 240  
 Gly Pro Ile Ala Phe Ala His Lys Arg Thr Ala Pro Ser Ser Val Leu  
 245 250 255  
 Thr Thr Gly Ser Gln Ala Gln Cys Thr Ser Tyr Phe Ile Glu Pro Val  
 260 265 270  
 Gln Trp Met Glu Ser Thr Leu Leu Gly Val Met Asp Gly Gln Leu Leu  
 275 280 285  
 Cys Pro Lys Cys Ser Ala Lys Leu Gly Ser Phe Asn Trp Tyr Gly Glu  
 290 295 300  
 Gln Cys Ser Cys Gly Arg Trp Ile Thr Pro Ala Phe Gln Ile His Lys  
 305 310 315 320  
 Asn Arg Val Asp Glu Met Lys Met Leu Pro Ala Leu Gly Ser Gln Thr  
 325 330 335  
 Lys Lys Leu

<210> 17  
 <211> 904  
 <212> DNA  
 <213> Homo sapiens

<400> 17  
 gtgttccgct caggcagagt cctgccccctg caccactcc cccattcccg gccccagggc 60  
 atgccccagg atggactcac tgcagaagca ggacctccgg aggcccaaga tccatggggc 120  
 agtccaggca tctccctacc agccggccac attggcttcg ctgcagcgct tgctgtgggt 180  
 ccgtcaggct gccacactga accatatcga tgaggctcg cccagccct tcctgggaga 240  
 tgcgtacgca gcccgggaca agagcaagct gatccagctg ggaatcaccc acgttgtgaa 300  
 tgccgctgca ggcaagttcc aggtggacac aggtgccaaa ttctaccgtg gaatgtccct 360  
 ggagactat ggcattgagg cggacaccaa ccccttctc gacctcagtg tctactttct 420  
 gcctgttgcg cgtatacatcc gagctgccct cagtgttccc caaggccgc tgctggta 480  
 ctgtgccatg gggtaagcc gctctgccac acttgtcctg gccttcctca tgatctatga 540  
 gaacatgacg ctggtagagg ccatccagac ggtgcaggcc caccgcaata tctgccctaa 600  
 ctcaggcttc ctccggcagc tccaggttct ggacaaccga ctggggcggg agacggggcg 660  
 gttctgatct ggcaaggcagc caggatccct gacccttggc ccaacccac cagcctggcc 720  
 ctggaaacag caggctctgc tgtttctagt gaccctgaga tgtaaacagc aagtgggggc 780  
 tgaggcagag gcagggatag ctgggtggtg acctcttagc gggtgattt ccctgaccca 840  
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 904  
 tcat

<210> 18  
 <211> 198  
 <212> PRT  
 <213> Homo sapiens

<400> 18  
 Met Asp Ser Leu Gln Lys Gln Asp Leu Arg Arg Pro Lys Ile His Gly  
 1 5 10 15  
 Ala Val Gln Ala Ser Pro Tyr Gln Pro Pro Thr Leu Ala Ser Leu Gln  
 20 25 30  
 Arg Leu Leu Trp Val Arg Gln Ala Ala Thr Leu Asn His Ile Asp Glu  
 35 40 45  
 Val Trp Pro Ser Leu Phe Leu Gly Asp Ala Tyr Ala Ala Arg Asp Lys  
 50 55 60  
 Ser Lys Leu Ile Gln Leu Gly Ile Thr His Val Val Asn Ala Ala Ala  
 65 70 75 80  
 Gly Lys Phe Gln Val Asp Thr Gly Ala Lys Phe Tyr Arg Gly Met Ser  
 85 90 95  
 Leu Glu Tyr Tyr Gly Ile Glu Ala Asp Asp Asn Pro Phe Phe Asp Leu  
 100 105 110  
 Ser Val Tyr Phe Leu Pro Val Ala Arg Tyr Ile Arg Ala Ala Leu Ser  
 115 120 125  
 Val Pro Gln Gly Arg Val Leu Val His Cys Ala Met Gly Val Ser Arg  
 130 135 140  
 Ser Ala Thr Leu Val Leu Ala Phe Leu Met Ile Tyr Glu Asn Met Thr  
 145 150 155 160  
 Leu Val Glu Ala Ile Gln Thr Val Gln Ala His Arg Asn Ile Cys Pro  
 165 170 175  
 Asn Ser Gly Phe Leu Arg Gln Leu Gln Val Leu Asp Asn Arg Leu Gly  
 180 185 190  
 Arg Glu Thr Gly Arg Phe  
 195

<210> 19  
<211> 908  
<212> DNA  
<213> Homo sapiens

<400> 19  
gtgagaggag acagaaaagag ggtgggtggcc gatacgctgg cctctttctc caacacccat 60  
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ccagcgtaga gagacacctgg accagccgcc ttgatgacag catccgcgtc ctccctttca 180  
tcatctcagg gtgtccagca gccctccatc tacagcttct cccaaataac cagaagcttg 240  
tttctcagca atggtgtggc cgccaaacgc aaactccctc tgtccagcaa tcgcattacc 300  
gccattgtca atgcctcggt ggaagtggtc aacgtattct tcgagggcat tcagttacata 360  
aaggtgcctg ttaccgatgc tcgtgactcg cgtctctacg acttttttga ccccatggct 420  
gatcttatcc acaccatcga tatgaggcag ggcgcgtacgc tgctgcactg catggctgga 480  
gtgagccgtt ccgcctcact gtgccttgcg tacctcatga aataccactc catgtcgctg 540  
ctggacgccc atacatggac caagtgcgc cggcccatca tccggcccaa caacggcttt 600  
tggaaacagc tcataatta cgaattcaag ctgtttaata acaacaccgt ggcgtatgatc 660

aactcgccgg taggtaacat ccctgacatc tatgagaagg acctacgtat gatgatatca 720  
 atgtaagcca tcccgccag cccctgacat ctgccatcgatcttgcacca agactgaact 780  
 ttgaacactg acatttgtt agtaaaagaaa accggatggt gccttggtaa agggcaagaa 840  
 aaaagggagg gggttggagt tttgaacgta gtaaggccta ccttaataga attaaattca 900  
 tgaaaacat 908

<210> 20  
<211> 190  
<212> PRT  
<213> Homo sapiens

<400> 20  
Met Thr Ala Ser Ala Ser Ser Phe Ser Ser Ser Gln Gly Val Gln Gln  
1 5 10 15  
Pro Ser Ile Tyr Ser Phe Ser Gln Ile Thr Arg Ser Leu Phe Leu Ser  
20 25 30  
Asn Gly Val Ala Ala Asn Asp Lys Leu Leu Leu Ser Ser Asn Arg Ile  
35 40 45  
Thr Ala Ile Val Asn Ala Ser Val Glu Val Val Asn Val Phe Phe Glu  
50 55 60  
Gly Ile Gln Tyr Ile Lys Val Pro Val Thr Asp Ala Arg Asp Ser Arg  
65 70 75 80  
Leu Tyr Asp Phe Phe Asp Pro Ile Ala Asp Leu Ile His Thr Ile Asp  
85 90 95  
Met Arg Gln Gly Arg Thr Leu Leu His Cys Met Ala Gly Val Ser Arg  
100 105 110  
Ser Ala Ser Leu Cys Leu Ala Tyr Leu Met Lys Tyr His Ser Met Ser  
115 120 125  
Leu Leu Asp Ala His Thr Trp Thr Lys Ser Arg Arg Pro Ile Ile Arg  
130 135 140  
Pro Asn Asn Gly Phe Trp Glu Gln Leu Ile Asn Tyr Glu Phe Lys Leu  
145 150 155 160  
Phe Asn Asn Asn Thr Val Arg Met Ile Asn Ser Pro Val Gly Asn Ile  
165 170 175  
Pro Asp Ile Tyr Glu Lys Asp Leu Arg Met Met Ile Ser Met  
180 185 190

<210> 21  
<211> 775  
<212> DNA  
<213> Homo sapiens

<400> 21  
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gacgcagcct tcgtgcttcg ctgactgctg accactgacc caccgccttg atgacagcac 120

cctcggtgtgc cttcccagtt cagttccggc agccctcagt cagcggcctc tcgcagataa 180  
 ccaaaaaggct gtatatcagc aatgggtgtgg ccgccaacaa caagctcatg ctgtcttagca 240  
 accagatcac catggtcatac aatgtctcag tggaggttagt gaacacccatg tatgaggata 300  
 tccagtgacat gcaggtaccc gtggctgact cccctaactc acgtctctgt gacttctttg 360  
 accctattgc tgaccatatac cacagcgtgg agatgaagca gggccgtact ttgctgcact 420  
 gtgctgctgg tggagccgc tcagctgccc tggcctcgc ctacctcatg aagtaccacg 480  
 ccatgtccct gctggacgccc cacacgtgga ccaagtcatac ccggcccatc atccgaccca 540  
 acagcgcctt ttgggagcag ctcataactc atgagttcca attgttggc aagaacactg 600  
 tgcacatggc cagttccccca gtggaatga tccctgacat ctatgagaag gaagtccgtt 660  
 tgatgattcc actgtgagcc atcccacgag cccctgcatt ggagtcaagag gtacagatct 720  
 attgttgcatac ttacaccaactt gaacattcta ctgggttga tacag 775

<210> 22  
<211> 188  
<212> PRT  
<213> Homo sapiens

<400> 22
Met Thr Ala Pro Ser Cys Ala Phe Pro Val Gln Phe Arg Gln Pro Ser
1 5 10 15
Val Ser Gly Leu Ser Gln Ile Thr Lys Ser Leu Tyr Ile Ser Asn Gly
20 25 30
Val Ala Ala Asn Asn Lys Leu Met Leu Ser Ser Asn Gln Ile Thr Met
35 40 45
Val Ile Asn Val Ser Val Glu Val Val Asn Thr Leu Tyr Glu Asp Ile
50 55 60
Gln Tyr Met Gln Val Pro Val Ala Asp Ser Pro Asn Ser Arg Leu Cys
65 70 75 80
Asp Phe Phe Asp Pro Ile Ala Asp His Ile His Ser Val Glu Met Lys
85 90 95
Gln Gly Arg Thr Leu Leu His Cys Ala Ala Gly Val Ser Arg Ser Ala
100 105 110
Ala Leu Cys Leu Ala Tyr Leu Met Lys Tyr His Ala Met Ser Leu Leu
115 120 125
Asp Ala His Thr Trp Thr Lys Ser Cys Arg Pro Ile Ile Arg Pro Asn
130 135 140
Ser Gly Phe Trp Glu Gln Leu Ile His Tyr Glu Phe Gln Leu Phe Gly
145 150 155 160
Lys Asn Thr Val His Met Val Ser Ser Pro Val Gly Met Ile Pro Asp
165 170 175
Ile Tyr Glu Lys Glu Val Arg Leu Met Ile Pro Leu
180 185

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<210> 23
<211> 1251
<212> DNA
<213> Homo sapiens

<400> 23
tgggcgcggc catgttggag gctccgggcc cgagtgtatgg ctgcgagctc agcaacccca 60
gcgcgcaggcag agtcagctgt gccgggcaga tgctggaaagt gcagccagga ttgttattcg 120
gtggggccgc ggcgcgtcgcg gagccagatc acctgaggaga agcgggcatac acggccgtgc 180
taacagtggc ctcggaggag cccagttca aggccggggcc tggggtcgag gatctatggc 240
gcctttcggt gccagcgctg gacaaaacccg agacggaccc actcagccat ctggaccggt 300
gcgtggccctt catcggtcag gcccgcgtg aggccgtgc ggtgttggtg cactgtcatg 360
caggagtcag tcgaagtgtg gccataataa ctgttttct catgaagact gaccaacttc 420
cctttaaaaa agcctatgaa aagctccaga ttctcaaacc agaggctaag atgaatgggg 480
ggttttagtg gcaactgaaa ttataccagg caatgggata tgaagtggat acctctatgt 540
caatttataa gcaatatcg ttacaaaagg ttacagagaaa gtatccagaa ttgcagaatt 600
taccccaaga actctttctt gttgacccaa ctaccgtttc acaaggattg aaagatgagg 660
ttctctacaa gttagaaaaag tgcaggcgat cattatttcg aagttctatg attctggatc 720
accgtgaagg aagtggaccc atagcccttgc cccacaagag aatgacacca tcttccatgc 780
ttaccacagg gagccaagct caatgtacat cttatttcat tgaacctgta cagtggatgg 840
aatctgcctt gttggagtg atggatggac agcttctttc cccaaaatgc agtgccaagt 900
tgggttcctt caactggatg ggtgaacagt gctttgtgg taggtggata acacactgtt 960
ttcaaataca taagaataga gtggatgaaa tgaaaatatt gcctgttttgc ggtacacaaa 1020
cagaaaaaat atgaacatga tattttatag ctgggaaaga aacttgcaga tggatgtgc 1080
tgccttgc tcttatcatt catggcagat tggtagtgc ttcaacattt catttggaaat 1140
gggagaagat aaaatcactt gatgtaacct ggaaaactatg ctttacatgg caatcaaagc 1200
cttttgcata tgcacatattt atttgatatt aaaatctttt ataaccagaa a 1251
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<210> 24
<211> 340
<212> PRT
<213> Homo sapiens

<400> 24
Met Leu Glu Ala Pro Gly Pro Ser Asp Gly Cys Glu Leu Ser Asn Pro
      1           5                   10                  15
Met Leu Glu Ala Pro Gly Pro Ser Asp Gly Cys Glu Leu Ser Asn Pro
      1           5                   10                  15
Ser Ala Ser Arg Val Ser Cys Ala Gly Gln Met Leu Glu Val Gln Pro
      20          25                   30
Ser Ala Ser Arg Val Ser Cys Ala Gly Gln Met Leu Glu Val Gln Pro
      20          25                   30
Gly Leu Tyr Phe Gly Gly Ala Ala Ala Val Ala Glu Pro Asp His Leu
      35          40                   45
Gly Leu Tyr Phe Gly Gly Ala Ala Ala Val Ala Glu Pro Asp His Leu
      35          40                   45
Arg Glu Ala Gly Ile Thr Ala Val Leu Thr Val Asp Ser Glu Glu Pro
      50          55                   60
Arg Glu Ala Gly Ile Thr Ala Val Leu Thr Val Asp Ser Glu Glu Pro
      50          55                   60
Ser Phe Lys Ala Gly Pro Gly Val Glu Asp Leu Trp Arg Leu Phe Val
      65          70                   75                  80
Ser Phe Lys Ala Gly Pro Gly Val Glu Asp Leu Trp Arg Leu Phe Val
      65          70                   75                  80
Pro Ala Leu Asp Lys Pro Glu Thr Asp Leu Leu Ser His Leu Asp Arg
      85          90                   95
Pro Ala Leu Asp Lys Pro Glu Thr Asp Leu Leu Ser His Leu Asp Arg
      85          90                   95
Cys Val Ala Phe Ile Gly Gln Ala Arg Ala Glu Gly Arg Ala Val Leu
      100         105                  110
Cys Val Ala Phe Ile Gly Gln Ala Arg Ala Glu Gly Arg Ala Val Leu
      100         105                  110
Val His Cys His Ala Gly Val Ser Arg Ser Val Ala Ile Ile Thr Ala
      115         120                  125

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Phe Leu Met Lys Thr Asp Gln Leu Pro Phe Glu Lys Ala Tyr Glu Lys  
 130 135 140  
 Leu Gln Ile Leu Lys Pro Glu Ala Lys Met Asn Glu Gly Phe Glu Trp  
 145 150 155 160  
 Gln Leu Lys Leu Tyr Gln Ala Met Gly Tyr Glu Val Asp Thr Ser Ser  
 165 170 175  
 Ala Ile Tyr Lys Gln Tyr Arg Leu Gln Lys Val Thr Glu Lys Tyr Pro  
 180 185 190  
 Glu Leu Gln Asn Leu Pro Gln Glu Leu Phe Ala Val Asp Pro Thr Thr  
 195 200 205  
 Val Ser Gln Gly Leu Lys Asp Glu Val Leu Tyr Lys Cys Arg Lys Cys  
 210 215 220  
 Arg Arg Ser Leu Phe Arg Ser Ser Ser Ile Leu Asp His Arg Glu Gly  
 225 230 235 240  
 Ser Gly Pro Ile Ala Phe Ala His Lys Arg Met Thr Pro Ser Ser Met  
 245 250 255  
 Leu Thr Thr Gly Arg Gln Ala Gln Cys Thr Ser Tyr Phe Ile Glu Pro  
 260 265 270  
 Val Gln Trp Met Glu Ser Ala Leu Leu Gly Val Met Asp Gly Gln Leu  
 275 280 285  
 Leu Cys Pro Lys Cys Ser Ala Lys Leu Gly Ser Phe Asn Trp Tyr Gly  
 290 295 300  
 Glu Gln Cys Ser Cys Gly Arg Trp Ile Thr Pro Ala Phe Gln Ile His  
 305 310 315 320  
 Lys Asn Arg Val Asp Glu Met Lys Ile Leu Pro Val Leu Gly Ser Gln  
 325 330 335  
 Thr Gly Lys Ile  
 340

<210> 25  
 <211> 687  
 <212> DNA  
 <213> Homo sapiens

<400> 25  
 gggccctgatccccata tagatcctca gggcccagaa gcagactctt cggcgccgc 60  
 catgggaccgc tcagaagctg ggccgcgcgg ggccgcctcg cccgtaccgc caccgttgt 120  
 gcgcgctcgcc ccctcactct tcctcggag cgccgcgagcc gcgggcgcgg aggagcagct 180  
 ggcgcgcgcgg ggagtcaactc tgcgtccgc cgtctccgc cagcagcccg gccccgcgc 240  
 gcccgcgtgc gcagagctgc gcgtccccgt gttcgacgc acggctgagg acctgctggc 300  
 gcacctggag cccacgtgcg cccatggaa ggcgcgggtg cgccgcggcg gccctgcct 360  
 agtctactgc aagaacggcc gcagccagct cggccgcgtc tgcaccgcgt acctcatgcg 420  
 gcaccgcggc ctcagcctgg cgaaggcatt ccagatggtg aagagcgctc gccccgttagc 480

agaaccgaac ccgggcttct ggtctcagct ccagaagtat gaggaggccc tccaggcccc 540  
gtcctgcctg cagggagagc ccccagcctt agggttgggc cctgaggcctt gaagcttcaa 600  
ggcctgtgc ctggaggaag gatgtccctg cactgataca gaaggctggt ctttaccctt 660  
cttcctcact gtcatatcga gttttcc 687

<210> 26  
<211> 176  
<212> PRT  
<213> *Homo sapiens*

<400> 26  
Met Gly Pro Ser Glu Ala Gly Arg Arg Gly Ala Ala Ser Pro Val Pro  
1 5 10 15

Pro Pro Leu Val Arg Val Ala Pro Ser Leu Phe Leu Gly Ser Ala Arg  
20 25 30

Ala Ala Gly Ala Glu Glu Gln Leu Ala Arg Ala Gly Val Thr Leu Cys  
35 40 45

Val Asn Val Ser Arg Gln Gln Pro Gly Pro Arg Ala Pro Gly Val Ala  
50 55 60

Glu	Leu	Arg	Val	Pro	Val	Phe	Asp	Asp	Pro	Ala	Glu	Asp	Leu	Leu	Ala
65					70					75					80

His Leu Glu Pro Thr Cys Ala Ala Met Glu Ala Ala Val Arg Ala Gly  
85 90 95

Gly Ala Cys Leu Val Tyr Cys Lys Asn Gly Arg Ser Gln Leu Gly Ala  
100 105 110

Val Cys Thr Ala Tyr Leu Met Arg His Arg Gly Leu Ser Leu Ala Lys  
115 120 125

Ala Phe Gln Met Val Lys Ser Ala Arg Pro Val Ala Glu Pro Asn Pro  
130 135 140

Gly Phe Trp Ser Gln Leu Gln Lys Tyr Glu Glu Ala Leu Gln Ala Gln  
 145                    150                    155                    160

Ser Cys Leu Gln Gly Glu Pro Pro Ala Leu Gly Leu Gly Pro Glu Ala  
165 170 175

<210> 27  
<211> 901  
<212> DNA  
<213> *Homo sapiens*

gactcatatt cttaatgttg catatggagt taaaaatgct ttccctcagtg actttacata 420  
 taagagcatt tctatattgg atctgcctga aaccaacatc ctgtcttatt ttccagaatg 480  
 ttttgaattt attgaagaag caaaaagaaa agatggagtg gttcttgttc attgtaatgc 540  
 aggcgttcc agggctgctg caattgtaat aggttccctg atgaattctg aacaaacctc 600  
 atttaccagt gcttttctt tggtaaaaaa tgcaagacct tccatatgtc caaattctgg 660  
 cttcatggag cagttcgtta cataatcaaga gggcaaagaa agcaataagt gtgacagaat 720  
 acaggagaac agttcatgag ttgcattgtta gcagacaatg gacaactgtta gtttctgaat 780  
 tgacttctat agccatctt tccctttttt ggagagtaga ctagaaaaat tccctttttt 840  
 ctcttgccctt ttttatgcat aaatggaggt caatctgatt gtcctgacct actgtataaaa 900  
 g 901

<210> 28  
 <211> 217  
 <212> PRT  
 <213> Homo sapiens

<400> 28  
 Met Tyr Ser Leu Asn Gln Glu Ile Lys Ala Phe Ser Arg Asn Asn Leu  
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 Arg Lys Gln Cys Thr Arg Val Thr Thr Leu Thr Gly Lys Lys Ile Ile  
 20 25 30  
 Glu Thr Trp Lys Asp Ala Arg Ile His Val Val Glu Glu Val Glu Pro  
 35 40 45  
 Ser Ser Gly Gly Cys Gly Tyr Val Gln Asp Leu Ser Ser Asp Leu  
 50 55 60  
 Gln Val Gly Val Ile Lys Pro Trp Leu Leu Leu Gly Ser Gln Asp Ala  
 65 70 75 80  
 Ala His Asp Leu Asp Thr Leu Lys Asn Lys Val Thr His Ile Leu  
 85 90 95  
 Asn Val Ala Tyr Gly Val Glu Asn Ala Phe Leu Ser Asp Phe Thr Tyr  
 100 105 110  
 Lys Ser Ile Ser Ile Leu Asp Leu Pro Glu Thr Asn Ile Leu Ser Tyr  
 115 120 125  
 Phe Pro Glu Cys Phe Glu Phe Ile Glu Glu Ala Lys Arg Lys Asp Gly  
 130 135 140  
 Val Val Leu Val His Cys Asn Ala Gly Val Ser Arg Ala Ala Ala Ile  
 145 150 155 160  
 Val Ile Gly Phe Leu Met Asn Ser Glu Gln Thr Ser Phe Thr Ser Ala  
 165 170 175  
 Phe Ser Leu Val Lys Asn Ala Arg Pro Ser Ile Cys Pro Asn Ser Gly  
 180 185 190  
 Phe Met Glu Gln Leu Arg Thr Tyr Gln Glu Gly Lys Glu Ser Asn Lys  
 195 200 205

Cys Asp Arg Ile Gln Glu Asn Ser Ser  
210 215

<210> 29  
<211> 2050  
<212> DNA  
<213> Homo sapiens

<220>  
<221> modified\_base  
<222> (1954)  
<223> a, c, g, t, other or unknown

<220>  
<221> modified\_base  
<222> (2010)  
<223> a, c, g, t, other or unknown

<220>  
<221> modified\_base  
<222> (2032)  
<223> a, c, g, t, other or unknown

<400> 29  
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tctgcagaat tcgccttac gattnagggt aactataga aggtacgcct gcaggtaccg 120  
gtccggaaatt cccgggtcga cccacgcgtc cgcaatgaag ccgagtgaat gggggctgaa 180  
tgtgcgagtc catacgctgaa gaggagcgc agatggtgaa ggaatacact tatttatgaa 240  
actgtcttga gttcttcttgc aattggcagt tttcagccctc ctcatgcctc cgtctccccc 300  
agacgcacagg gtagttagtgg cactatctag gcccgtccga cctcaggatc tcaacccccc 360  
tttagactct atttaccttgc gctctgccaa cccaggcagt aacagccacc ctcctgtcat 420  
cgccaccacc gttgtgtccc tcaaggctgc gaatctgacg tatatgcct catccagcgg 480  
ctctgcccgc tcgctgaatt gtggatgcag cagtgcgcgc tgctgcactg tggcaaccta 540  
cgacaaggac aatcaggccc aaacccaagc cattgcccgc ggcaccacca ccaactgcct 600  
cggaacctct accacctgcc ctgcttaacca gatggtaaac aataatgaga atacaggctc 660  
tctaagtccca tcaagtgggg tgggcagccc tggcgtcaggg acccccaagc agctagccag 720  
catcaaaaata atctacccca atgacttgc aaagaagatg accaaatgca gcaagagtc 780  
cctgcccagt cagggccctg tcattcattga ctgcaggcccc ttcatggagt acaacaagag 840  
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gcagggcaag atcaactgtcc tagacttgc ttctgttagg gaaggcaagg actctttcaa 960  
gaggatctt tccaaagaaaa ttatagttt tgatgagaat accaatgagc caagccgagt 1020  
gatgccctcc cagccacttc acatagtcct cgagtcctcg aagagagaag gcaaaagaacc 1080  
tctgggtttg aaaggtggac tttagttt taagcagaac cataaaaacc tctgtgacaaa 1140  
ctccctccag ctccaagagt gcccggaggt gggggccggc gcatccgggg ctcgagctt 1200  
gctacccatcg cccatccccca ccacccctga catcgagaac gctgagctca ccccccattt 1260  
gcccttccttgc ttctttggca atgagcaggta tgcgtggac ctggacacca tgcagcggct 1320  
gaacatcgcc tacgttcatca acgttcacccat tcatttccctt ctctaccact atgagaaaagg 1380  
cctgttcaac tacaagcggc tgccaagcac tgacagcaac aagcagaacc tgcggcagta 1440  
ctttgaagag gcttttggat tcatttggat agctcaccat gttggaaagg ggcttctcat 1500  
ccactgcccag gctgggggtgt cccgcgtccgc caccatcgat atcgcttact tgatgaagca 1560  
cactcggtatg accatgactg atgcttataa atttgcataa ggcaaaacgcac caattatctc 1620  
cccaaaacccat aacttcatgg ggcagggtgc agagttcgat gaagaccta acaacgggt 1680  
gacaccggaga atcccttacac caaagctgtat gggcgtggat acgggtgtgt gacaatggtc 1740  
tggatggaaa ggattgctgc tctccattat gagacaatgaa ggaaggagga tggattctgg 1800  
ttttttttct ttcttttttt tttgttagttt ggatgaaatggtt ttgtgaatgg aaacaaaccc 1860  
ggtaaacaat tttatttttt acaagttgtaa gaagactata cttttgtatgc cattgagatt 1920  
caccttccac aaactggcca aattaaggat gttnaagaag taatttttt taagcccaac 1980

cattaaaaat ttaatacacaac ttggtttctn ccccttttc cttaaagct antttgtaaa 2040  
agtttatgag 2050

<210> 30  
<211> 482  
<212> PRT  
<213> *Homo sapiens*

<400> 30  
Met Pro Pro Ser Pro Leu Asp Asp Arg Val Val Val Ala Leu Ser Arg  
1 5 10 15

Pro Val Arg Pro Gln Asp Leu Asn Leu Cys Leu Asp Ser Ser Tyr Leu  
                  20                 25                                 30

Gly Ser Ala Asn Pro Gly Ser Asn Ser His Pro Pro Val Ile Ala Thr  
35 40 45

Thr	Val	Val	Ser	Leu	Lys	Ala	Ala	Asn	Leu	Thr	Tyr	Met	Pro	Ser	Ser
50					55						60				

Ser Gly Ser Ala Arg Ser Leu Asn Cys Gly Cys Ser Ser Ala Ser Cys  
65 70 75 80

Cys Thr Val Ala Thr Tyr Asp Lys Asp Asn Gln Ala Gln Thr Gln Ala  
85 90 95

Ile Ala Ala Gly Thr Thr Thr Thr Ala Ile Gly Thr Ser Thr Thr Cys  
                   100                  105                  110

Pro Ala Asn Gln Met Val Asn Asn Asn Glu Asn Thr Gly Ser Leu Ser  
115 120 125

Pro Ser Ser Gly Val Gly Ser Pro Val Ser Gly Thr Pro Lys Gln Leu  
130 135 140

Ala Ser Ile Lys Ile Ile Tyr Pro Asn Asp Leu Ala Lys Lys Met Thr  
145 150 155 160

Lys Cys Ser Lys Ser His Leu Pro Ser Gin Gly Pro Val Ile Ile Asp  
165 170 175

Cys Arg Pro Phe Met Glu Tyr Asn Lys Ser His Ile Gin Gly Ala Val  
180 185 190

His Ile Asn Cys Ala Asp Lys Ile Ser Arg Arg Arg Leu Gin Gin Gly  
195 200 205

Lys Ile Thr Val Leu Asp Leu Ile Ser Cys Arg Glu Gly Lys Asp Ser  
210 215 220

Phe Lys Arg Ile Phe Ser Lys Glu Ile Ile Val Tyr Asp Glu Asn Thr  
225 230 235 240

Asn Glu Pro Ser Arg Val Met Pro Ser Gln Pro Leu His Ile Val Leu  
245 250 255

Glu Ser Leu Lys Arg Glu Gly Lys Glu Pro Leu Val Leu Lys Gly Gly  
 260 265 270

Leu Ser Ser Phe Lys Gln Asn His Glu Asn Leu Cys Asp Asn Ser Leu  
 275 280 285

Gln Leu Gln Glu Cys Arg Glu Val Gly Gly Ala Ser Gly Ala Ser  
 290 295 300

Ser Leu Leu Pro Gln Pro Ile Pro Thr Thr Pro Asp Ile Glu Asn Ala  
 305 310 315 320

Glu Leu Thr Pro Ile Leu Pro Phe Leu Phe Leu Gly Asn Glu Gln Asp  
 325 330 335

Val Arg Asp Leu Asp Thr Met Gln Arg Leu Asn Ile Gly Tyr Val Ile  
 340 345 350

Asn Val Thr Thr His Leu Pro Leu Tyr His Tyr Glu Lys Gly Leu Phe  
 355 360 365

Asn Tyr Lys Arg Leu Pro Ser Thr Asp Ser Asn Lys Gln Asn Leu Arg  
 370 375 380

Gln Tyr Phe Glu Glu Ala Phe Glu Phe Ile Glu Glu Ala His Gln Cys  
 385 390 395 400

Gly Lys Gly Leu Leu Ile His Cys Gln Ala Gly Val Ser Arg Ser Ala  
 405 410 415

Thr Ile Val Ile Ala Tyr Leu Met Lys His Thr Arg Met Thr Met Thr  
 420 425 430

Asp Ala Tyr Lys Phe Val Lys Gly Lys Arg Pro Ile Ile Ser Pro Asn  
 435 440 445

Leu Asn Phe Met Gly Gln Leu Leu Glu Phe Glu Glu Asp Leu Asn Asn  
 450 455 460

Gly Val Thr Pro Arg Ile Leu Thr Pro Lys Leu Met Gly Val Glu Thr  
 465 470 475 480

Val Val

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 <211> 1026  
 <212> DNA  
 <213> Homo sapiens

<400> 31  
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ttccagggc aggaggcaggg gcagggcag ggcagggag agccctgcat ttctctacg 960  
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gcctga 1026

<210> 32  
<211> 341  
<212> PRT  
<213> Homo sapiens

<400> 32  
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His Leu Tyr Leu Gly Ser Glu Trp Asn Ala Ala Asn Leu Glu Glu Leu  
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Gln Arg Asn Arg Val Thr His Ile Leu Asn Met Ala Arg Glu Ile Asp  
35 40 45  
Asn Phe Tyr Pro Glu Arg Phe Thr Tyr His Asn Val Arg Leu Trp Asp  
50 55 60  
Glu Glu Ser Ala Gln Leu Leu Pro His Trp Lys Glu Thr His Arg Phe  
65 70 75 80  
Ile Glu Ala Ala Arg Ala Gln Gly Thr His Val Leu Val His Cys Lys  
85 90 95  
Met Gly Val Ser Arg Ser Ala Ala Thr Val Leu Ala Tyr Ala Met Lys  
100 105 110  
Gln Tyr Glu Cys Ser Leu Glu Gln Ala Leu Arg His Val Gln Glu Leu  
115 120 125  
Arg Pro Ile Ala Arg Pro Asn Pro Gly Phe Leu Arg Gln Leu Gln Ile  
130 135 140  
Tyr Gln Gly Ile Leu Thr Ala Ser Arg Gln Ser His Val Trp Glu Gln  
145 150 155 160  
Lys Val Gly Gly Val Ser Pro Glu Glu His Pro Ala Pro Glu Val Ser  
165 170 175  
Thr Pro Phe Pro Pro Leu Pro Pro Glu Pro Glu Gly Gly Glu Glu  
180 185 190  
Lys Val Val Gly Met Glu Glu Ser Gln Ala Ala Pro Lys Glu Glu Pro  
195 200 205

Gly Pro Arg Pro Arg Ile Asn Leu Arg Gly Val Met Arg Ser Ile Ser  
 210 215 220

Leu Leu Glu Pro Ser Leu Glu Leu Glu Ser Thr Ser Glu Thr Ser Asp  
 225 230 235 240

Met Pro Glu Val Phe Ser Ser His Glu Ser Ser His Glu Glu Pro Leu  
 245 250 255

Gln Pro Phe Pro Gln Leu Ala Arg Thr Lys Gly Gly Gln Gln Val Asp  
 260 265 270

Arg Gly Pro Gln Pro Ala Leu Lys Ser Arg Gln Ser Val Val Thr Leu  
 275 280 285

Gln Gly Ser Ala Val Val Ala Asn Arg Thr Gln Ala Phe Gln Glu Gln  
 290 295 300

Glu Gln Gly Gln Gly Gln Gly Glu Pro Cys Ile Ser Ser Thr  
 305 310 315 320

Pro Arg Phe Arg Lys Val Val Arg Gln Ala Ser Val His Asp Ser Gly  
 325 330 335

Glu Glu Gly Glu Ala  
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<210> 33  
 <211> 3995  
 <212> DNA  
 <213> Homo sapiens

<400> 33

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<210> 34  
<211> 777  
<212> PRT  
<213> *Homo sapiens*

<400> 34  
Met Phe Ser Leu Lys Pro Pro Lys Pro Thr Phe Arg Ser Tyr Phe Leu  
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Pro Pro Pro Gln Thr Asp Asp Lys Ile Asn Ser Glu Pro Lys Ile Lys  
20 25 30

Lys Leu Glu Pro Val Leu Leu Pro Gly Glu Ile Val Val Asn Glu Val  
     35                        40                        45

Asn Phe Val Arg Lys Cys Ile Ala Thr Asp Thr Ser Gln Tyr Asp Leu  
     50                        55                        60

Trp Gly Lys Leu Ile Cys Ser Asn Phe Lys Ile Ser Phe Ile Thr Asp  
     65                        70                        75                        80

Asp Pro Met Pro Leu Gln Lys Phe His Tyr Arg Asn Leu Leu Leu Gly  
     85                        90                        95

Glu His Asp Val Pro Leu Thr Cys Ile Glu Gln Ile Val Thr Val Asn  
     100                       105                       110

Asp His Lys Arg Lys Gln Lys Val Leu Gly Pro Asn Gln Lys Leu Lys  
     115                       120                       125

Phe Asn Pro Thr Glu Leu Ile Ile Tyr Cys Lys Asp Phe Arg Ile Val  
     130                       135                       140

Arg Phe Arg Phe Asp Glu Ser Gly Pro Glu Ser Ala Lys Lys Val Cys  
     145                       150                       155                       160

Leu Ala Ile Ala His Tyr Ser Gln Pro Thr Asp Leu Gln Leu Leu Phe  
     165                       170                       175

Ala Phe Glu Tyr Val Gly Lys Tyr His Asn Ser Ala Asn Lys Ile  
     180                       185                       190

Asn Gly Ile Pro Ser Gly Asp Gly Gly Gly Gly Gly Gly Asn  
     195                       200                       205

Gly Ala Gly Gly Ser Ser Gln Lys Thr Pro Leu Phe Glu Thr Tyr  
     210                       215                       220

Ser Asp Trp Asp Arg Glu Ile Lys Arg Thr Gly Ala Ser Gly Trp Arg  
     225                       230                       235                       240

Val Cys Ser Ile Asn Glu Gly Tyr Met Ile Ser Thr Cys Leu Pro Glu  
     245                       250                       255

Tyr Ile Val Val Pro Ser Ser Leu Ala Asp Gln Asp Leu Lys Ile Phe  
     260                       265                       270

Ser His Ser Phe Val Gly Arg Arg Met Pro Leu Trp Cys Trp Ser His  
     275                       280                       285

Ser Asn Gly Ser Ala Leu Val Arg Met Ala Leu Ile Lys Asp Val Leu  
     290                       295                       300

Gln Gln Arg Lys Ile Asp Gln Arg Ile Cys Asn Ala Ile Thr Lys Ser  
     305                       310                       315                       320

His Pro Gln Arg Ser Asp Val Tyr Lys Ser Asp Leu Asp Lys Thr Leu  
     325                       330                       335

Pro Asn Ile Gln Glu Val Gln Ala Ala Phe Val Lys Leu Lys Gln Leu  
           340                     345                     350

Cys Val Asn Glu Pro Phe Glu Glu Thr Glu Glu Lys Trp Leu Ser Ser  
           355                     360                     365

Leu Glu Asn Thr Arg Trp Leu Glu Tyr Val Arg Ala Phe Leu Lys His  
           370                     375                     380

Ser Ala Glu Leu Val Tyr Met Leu Glu Ser Lys His Leu Ser Val Val  
           385                     390                     395              400

Leu Gln Glu Glu Glu Gly Arg Asp Leu Ser Cys Cys Val Ala Ser Leu  
           405                     410                     415

Val Gln Val Met Leu Asp Pro Tyr Phe Arg Thr Ile Thr Gly Phe Gln  
           420                     425                     430

Ser Leu Ile Gln Lys Glu Trp Val Met Ala Gly Tyr Gln Phe Leu Asp  
           435                     440                     445

Arg Cys Asn His Leu Lys Arg Ser Glu Lys Glu Ser Pro Leu Phe Leu  
           450                     455                     460

Leu Phe Leu Asp Ala Thr Trp Gln Leu Leu Glu Gln Tyr Pro Ala Ala  
           465                     470                     475              480

Phe Glu Phe Ser Glu Thr Tyr Leu Ala Val Leu Tyr Asp Ser Thr Arg  
           485                     490                     495

Ile Ser Leu Phe Gly Thr Phe Leu Phe Asn Ser Pro His Gln Arg Val  
           500                     505                     510

Lys Gln Ser Thr Glu Phe Ala Ile Ser Lys Asn Ile Gln Leu Gly Asp  
           515                     520                     525

Glu Lys Gly Leu Lys Phe Pro Ser Val Trp Asp Trp Ser Leu Gln Phe  
           530                     535                     540

Thr Ala Lys Asp Arg Thr Leu Phe His Asn Pro Phe Tyr Ile Gly Lys  
           545                     550                     555              560

Ser Thr Pro Cys Ile Gln Asn Gly Ser Val Lys Ser Phe Lys Arg Thr  
           565                     570                     575

Lys Lys Ser Tyr Ser Ser Thr Leu Arg Gly Met Pro Ser Ala Leu Lys  
           580                     585                     590

Asn Gly Ile Ile Ser Asp Gln Glu Leu Leu Pro Arg Arg Asn Ser Leu  
           595                     600                     605

Ile Leu Lys Pro Lys Pro Asp Pro Ala Gln Gln Thr Asp Ser Gln Asn  
           610                     615                     620

Ser Asp Thr Glu Gln Tyr Phe Arg Glu Trp Phe Ser Lys Pro Ala Asn  
           625                     630                     635              640

Leu His Gly Val Ile Leu Pro Arg Val Ser Gly Thr His Ile Lys Leu  
 645 650 655

Trp Lys Leu Cys Tyr Phe Arg Trp Val Pro Glu Ala Gln Ile Ser Leu  
 660 665 670

Gly Gly Ser Ile Thr Ala Phe His Lys Leu Ser Leu Leu Ala Asp Glu  
 675 680 685

Val Asp Val Leu Ser Arg Met Leu Arg Gln Gln Arg Ser Gly Pro Leu  
 690 695 700

Glu Ala Cys Tyr Gly Glu Leu Gly Gln Ser Arg Met Tyr Phe Asn Ala  
 705 710 715 720

Ser Gly Pro His His Thr Asp Thr Ser Gly Thr Pro Glu Phe Leu Ser  
 725 730 735

Ser Ser Phe Pro Phe Ser Pro Val Gly Asn Leu Cys Arg Arg Ser Ile  
 740 745 750

Leu Gly Thr Pro Leu Ser Lys Phe Leu Ser Gly Ala Lys Ile Trp Leu  
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Ser Thr Glu Thr Leu Ala Asn Glu Asp  
 770 775

<210> 35

<211> 2353

<212> DNA

<213> Homo sapiens

<400> 35

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&lt;210&gt; 36

&lt;211&gt; 629

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 36

Met	Val	Pro	Pro	Lys	Leu	Gln	Glu	Ala	Phe	Glu	Pro	Phe	Asp	Leu	Lys
1					5				10			15			

His	Ala	Gly	Ala	His	Phe	Arg	Ala	Pro	Pro	Arg	Glu	Ser	Leu	Asp	His
					20				25			30			

Arg	Glu	Asn	Arg	Val	Phe	Arg	Gly	Phe	Ala	Pro	Pro	Asp	Lys	Arg	Asn
					35			40				45			

Glu	Gln	Ala	Gly	Ser	Ser	Ser	Ala	Val	Val	Ser	Val	Phe	Tyr	Val	Cys
					50			55				60			

Gly	Met	Ala	Gln	Tyr	Ser	Ser	Ser	Ser	Ser	Val	Ala	Gln	Gly	Ser	
	65				70				75			80			

Arg	Lys	Val	Glu	Asn	Val	Arg	Leu	Val	Asp	Arg	Val	Ser	Pro	Lys	Lys
					85				90			95			

Ala	Ala	Leu	Gly	Thr	Leu	Tyr	Leu	Thr	Ala	Thr	His	Val	Ile	Phe	Val
					100			105				110			

Glu	Asn	Ser	Pro	Asp	Ala	Arg	Lys	Glu	Thr	Trp	Ile	Leu	His	Ser	Gln
					115			120			125				

Ile	Ser	Thr	Ile	Glu	Lys	Gln	Ala	Thr	Thr	Ala	Thr	Gly	Cys	Pro	Leu
			130					135			140				

Leu	Ile	Arg	Cys	Lys	Asn	Phe	Gln	Ile	Ile	Gln	Leu	Ile	Ile	Pro	Gln
					145				150			155		160	

Glu	Arg	Asp	Cys	His	Asp	Val	Tyr	Ile	Ser	Leu	Ile	Arg	Leu	Ala	Arg
					165				170			175			

Pro Val Lys Tyr Glu Glu Leu Tyr Cys Phe Ser Phe Asn Pro Met Leu  
 180 185 190

Asp Lys Glu Glu Arg Glu Gln Gly Trp Val Leu Ile Asp Leu Ser Glu  
 195 200 205

Glu Tyr Thr Arg Met Gly Leu Pro Asn His Tyr Trp Gln Leu Ser Asp  
 210 215 220

Val Asn Arg Asp Tyr Arg Val Cys Asp Ser Tyr Pro Thr Glu Leu Tyr  
 225 230 235 240

Val Pro Lys Ser Ala Thr Ala His Ile Ile Val Gly Ser Ser Lys Phe  
 245 250 255

Arg Ser Arg Arg Arg Phe Pro Val Leu Ser Tyr Tyr Tyr Lys Asp Asn  
 260 265 270

His Ala Ser Ile Cys Arg Ser Ser Gln Pro Leu Ser Gly Phe Ser Ala  
 275 280 285

Arg Cys Leu Glu Asp Glu Gln Met Leu Gln Ala Ile Arg Lys Ala Asn  
 290 295 300

Pro Gly Ser Asp Phe Val Tyr Val Val Asp Thr Arg Pro Lys Leu Asn  
 305 310 315 320

Ala Met Ala Asn Arg Ala Ala Gly Lys Gly Tyr Glu Asn Glu Asp Asn  
 325 330 335

Tyr Ser Asn Ile Lys Phe Gln Phe Ile Gly Ile Glu Asn Ile His Val  
 340 345 350

Met Arg Asn Ser Leu Gln Lys Met Leu Glu Val Cys Glu Leu Lys Ser  
 355 360 365

Pro Ser Met Ser Asp Phe Leu Trp Gly Leu Glu Asn Ser Gly Trp Leu  
 370 375 380

Arg His Ile Lys Ala Ile Met Asp Ala Gly Ile Phe Ile Ala Lys Ala  
 385 390 395 400

Val Ser Glu Glu Gly Ala Ser Val Leu Val His Cys Ser Asp Gly Trp  
 405 410 415

Asp Arg Thr Ala Gln Val Cys Ser Val Ala Ser Leu Leu Asp Pro  
 420 425 430

His Tyr Arg Thr Leu Lys Gly Phe Met Val Leu Ile Glu Lys Asp Trp  
 435 440 445

Ile Ser Phe Gly His Lys Phe Asn His Arg Tyr Gly Asn Leu Asp Gly  
 450 455 460

Asp Pro Lys Glu Ile Ser Pro Val Ile Asp Gln Phe Ile Glu Cys Val  
 465 470 475 480

Trp Gln Leu Met Glu Gln Phe Pro Cys Ala Phe Glu Phe Asn Glu Arg  
485 490 495

Phe Leu Ile His Ile Gln His His Ile Tyr Ser Cys Gln Phe Gly Asn  
500 505 510

Phe Leu Cys Asn Ser Gln Lys Glu Arg Arg Glu Leu Lys Ile Gln Glu  
 515                    520                    525

Arg Thr Tyr Ser Leu Trp Ala His Leu Trp Lys Asn Arg Ala Asp Tyr  
530 535 540

Leu Asn Pro Leu Phe Arg Ala Asp His Ser Gln Thr Gln Gly Thr Phe  
545 550 555 560

His Leu Pro Thr Thr Pro Cys Asn Phe Met Tyr Lys Phe Trp Ser Gly  
565 570 575

Met Tyr Asn Arg Phe Glu Lys Gly Met Gln Pro Arg Gln Ser Val Thr  
               580                   585                   590

Asp Tyr Leu Met Ala Val Lys Glu Glu Thr Gln Gln Leu Glu Glu Glu  
595 600 605

Leu Glu Ala Leu Glu Glu Val Arg His Thr Cys Phe Val Asn Leu Phe  
610 615 620

Ser Val Leu Ile Ser  
625

<210> 37  
<211> 1200  
<212> DNA  
<213> *Homo sapiens*

&lt;210&gt; 38

&lt;211&gt; 400

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 38

Met	Asn	Glu	Ser	Pro	Asp	Pro	Asn	Ala	Leu	Ala	Gly	Val	Ile	Ile	Glu
1				5					10					15	

Arg	Ala	Pro	Ser	Asp	Ser	Pro	Gln	Thr	Asn	Glu	Phe	Lys	Gly	Ala	Thr
20							25					30			

Glu	Glu	Ala	Pro	Ala	Lys	Glu	Ser	Pro	His	Thr	Ser	Glu	Phe	Lys	Gly
35						40						45			

Ala	Ala	Leu	Val	Ser	Pro	Ile	Ser	Lys	Ser	Met	Leu	Glu	Arg	Leu	Ser
50						55				60					

Lys	Phe	Glu	Val	Glu	Asp	Ala	Glu	Asn	Val	Ala	Ser	Tyr	Asp	Ser	Lys
65						70				75			80		

Ile	Lys	Lys	Ile	Val	His	Ser	Ile	Val	Ser	Ser	Phe	Ala	Phe	Gly	Leu
85							90					95			

Phe	Gly	Val	Phe	Leu	Val	Leu	Leu	Asp	Val	Thr	Leu	Val	Leu	Ala	Asp
100							105				110				

Leu	Ile	Phe	Thr	Asp	Ser	Lys	Leu	Tyr	Ile	Pro	Ser	Glu	Tyr	Arg	Ser
115						120				125					

Ile	Ser	Leu	Ala	Ile	Ala	Leu	Phe	Phe	Leu	Met	Asp	Val	Leu	Leu	Arg
130						135				140					

Val	Phe	Val	Glu	Gly	Pro	Val	Tyr	Thr	Ile	Gly	Leu	Pro	Pro	Ser	Asp
145						150			155			160			

Leu	Arg	Ala	Gly	Lys	Glu	Glu	Thr	Val	Leu	Val	Arg	Glu	Arg	His	Gln
165						170					175				

Gln	Glu	Ser	Gln	Arg	Phe	Leu	Leu	Ser	Ile	Ile	Thr	Ile	Thr	Ile	
180								185			190				

Ile	Leu	Ile	Thr	Ile	Thr	Val	Thr	Val	Ile	Lys	Tyr	Phe	Asn	Leu	Thr
195						200				205					

Lys	Asn	Ile	Lys	Leu	Glu	Ile	Ser	Lys	Met	Val	Val	Phe	Ser	Lys	Glu
210						215				220					

Val	Asn	Glu	Trp	Met	Thr	Gln	Asp	Pro	Glu	Asn	Ile	Ile	Val	Ile	His
225						230			235			240			

Cys	Lys	Gly	Gly	Lys	Ile	Ile	Ile	Thr	Ile	Met	Asp	Phe	Lys	Glu	Val
245							250				255				

Cys	Thr	Thr	Gln	Tyr	Cys	Lys	Val	Val	Ser	Ser	Leu	Lys	Leu	Ile	Tyr
260							265				270				

Lys Phe Asn Val Val Pro Ile Lys Ile Leu Asn Val Lys Gly Arg Thr  
 275 280 285

Gly Thr Met Val Cys Ala Leu Leu Ile Ala Ser Glu Ile Phe Leu Thr  
 290 295 300

Ala Glu Glu Ser Leu Tyr Tyr Phe Gly Glu Arg Arg Thr Asp Lys Thr  
 305 310 315 320

His Ser Asn Lys Phe Gln Gly Val Glu Thr Pro Cys Gln Asn Arg Tyr  
 325 330 335

Val Gly Tyr Phe Ala Gln Val Lys His Leu Tyr Asn Gly Asn Ile Pro  
 340 345 350

Pro Arg Arg Ile Leu Phe Ile Lys Arg Phe Ile Ile Tyr Ser Thr Arg  
 355 360 365

Gly Val Gly Thr Gly Asp Val Cys Asp Leu Gln Phe Gln Ile Val Met  
 370 375 380

Glu Lys Lys Val Val Phe Ser Ser Thr Ser Leu Gly Asn Cys Ser Leu  
 385 390 395 400

<210> 39

<211> 694

<212> DNA

<213> Homo sapiens

<400> 39

gtggcccgaa aggccgcgag gccaggtagg tgcgatggc gtgcagcccc ccaacttctc 60  
 ctgggtgctt ccggccggc tggcggact ggcgctgccg cggctccccg cccactacca 120  
 gttccctgtt gacacctggcg tgcggcacct ggtgtccctg acggagcgcg ggccccctca 180  
 cagcgacaggc tgccccggcc tcaccctgca cccgcctgcgc atccccact tctgcccggc 240  
 ggccccggac cagatcgacc gttcgtgca gatcgtggac gaggccaacg cacggggaga 300  
 ggctgtggga gtgcactgtg ctctggctt tggccgcact ggcacccatgc tggcctgtta 360  
 cctggtaag gacgggggt tggctgcagg agatgccatt gctgaaatcc gacgactacg 420  
 acccgccccc atcgagaccc atgagcagga gaaagcagtc ttccagttct accagcgaac 480  
 gaaataaggg gccttagtac cttcttacca gcccctcact ccccttcccc atgttgtcga 540  
 tggggccaga gatgaaggaa agtgactaa agtattaaac cctctagctc ccattggctg 600  
 aagacactga agtagcccac ccctgcaggc aggtcctgtat tgaagggag gcttgtactg 660  
 ctttggaa taaatgagtt ttacgaacca ggaa 694

<210> 40

<211> 150

<212> PRT

<213> Homo sapiens

<400> 40

Met Gly Val Gln Pro Pro Asn Phe Ser Trp Val Leu Pro Gly Arg Leu  
 1 5 10 15

Ala Gly Leu Ala Leu Pro Arg Leu Pro Ala His Tyr Gln Phe Leu Leu  
 20 25 30

Asp Leu Gly Val Arg His Leu Val Ser Leu Thr Glu Arg Gly Pro Pro  
 35 40 45

His Ser Asp Ser Cys Pro Gly Leu Thr Leu His Arg Leu Arg Ile Pro  
 50 55 60

Asp Phe Cys Pro Pro Ala Pro Asp Gln Ile Asp Arg Phe Val Gln Ile  
 65 70 75 80

Val Asp Glu Ala Asn Ala Arg Gly Glu Ala Val Gly Val His Cys Ala  
 85 90 95

Leu Gly Phe Gly Arg Thr Gly Thr Met Leu Ala Cys Tyr Leu Val Lys  
 100 105 110

Glu Arg Gly Leu Ala Ala Gly Asp Ala Ile Ala Glu Ile Arg Arg Leu  
 115 120 125

Arg Pro Gly Pro Ile Glu Thr Tyr Glu Gln Glu Lys Ala Val Phe Gln  
 130 135 140

Phe Tyr Gln Arg Thr Lys  
 145 150

<210> 41

<211> 57

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<220>

<221> modified\_base

<222> (57)

<223> a, c, g, t, other or unknown

<400> 41

aagcagtggtaacaacgcag agtactttttttttttttttttttttttttvnn 57

<210> 42

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 42

aagtggcaac agagataacg cgtacgcggg

30

<210> 43

<211> 30

<212> DNA

<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic primer

<400> 43  
aagcagtggt aacaacgcag agtacgcggg

30

<210> 44  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic primer

<400> 44  
aagcagtggt aacaacgcag agt

23

<210> 45  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic primer

<400> 45  
aagtggcaac agagataacg cgt

23